

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : David White et al.
Serial No.: 09/195,896
Filed : November 19, 1998
Title : LEPTIN INDUCED GENES

Art Unit:
Examiner:

Box Sequence
Assistant Commissioner for Patents
Washington, DC 20231

VERIFIED STATEMENT UNDER 37 CFR § 1.821 (f)

I, Maureen Ruttle, declare that I personally prepared the paper and the computer-readable copies of the Sequence Listing filed herewith in the above-entitled case and that the content of both is the same.

I further declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of The United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Date: Nov 15, 1999

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Date of Deposit November 29, 1999
I hereby certify under 37 CFR 1.8(a) that this correspondence is being deposited with the United States Postal Service as **first class mail** with sufficient postage on the date indicated above and is addressed to the Assistant Commissioner for Patents, Washington, D.C. 20231.

Carrie A. Amonte

SEQUENCE LISTING

<110> White, David
Zhou, Jianghong
Tartaglia, Louis A.

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<140> US 09/195,896

<141> 1998-11-19

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<151> 1998-10-29

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Gly	His	Pro	Asn	Ser	Tyr	His	Phe	Lys	Tyr	Ile	Ile	Asn	Glu	Pro	Glu
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Lys	Cys	Gln	Glu	Lys	Ser	Pro	Phe	Leu	Ile	Leu	Leu	Ile	Ala	Ala	Glu
	145				150					155					160
Pro	Gly	Gln	Ile	Glu	Ala	Arg	Arg	Ala	Ile	Arg	Gln	Thr	Trp	Gly	Asn
				165				170						175	
Glu	Ser	Leu	Ala	Pro	Gly	Ile	Gln	Ile	Thr	Arg	Ile	Phe	Leu	Leu	Gly
			180				185						190		
Leu	Ser	Ile	Lys	Leu	Asn	Gly	Tyr	Leu	Gln	Arg	Ala	Ile	Leu	Glu	Glu
		195					200					205			
Ser	Arg	Gln	Tyr	His	Asp	Ile	Ile	Gln	Gln	Glu	Tyr	Leu	Asp	Thr	Tyr
	210					215					220				
Tyr	Asn	Leu	Thr	Ile	Lys	Thr	Leu	Met	Gly	Met	Asn	Trp	Val	Ala	Thr
225					230					235					240
Tyr	Cys	Pro	His	Ile	Pro	Tyr	Val	Met	Lys	Thr	Asp	Ser	Asp	Met	Phe
				245					250					255	
Val	Asn	Thr	Glu	Tyr	Leu	Ile	Asn	Lys	Leu	Leu	Lys	Pro	Asp	Leu	Pro
			260					265					270		
Pro	Arg	His	Asn	Tyr	Phe	Thr	Gly	Tyr	Leu	Met	Arg	Gly	Tyr	Ala	Pro
		275					280					285			
Asn	Arg	Asn	Lys	Asp	Ser	Lys	Trp	Tyr	Met	Pro	Pro	Asp	Leu	Tyr	Pro
	290					295					300				

Ser Glu Arg Tyr Pro Val Phe Cys Ser Gly Thr Gly Tyr Val Phe Ser
 305 310 315 320
 Gly Asp Leu Ala Glu Lys Ile Phe Lys Val Ser Leu Gly Ile Arg Arg
 325 330 335
 Leu His Leu Glu Asp Val Tyr Val Gly Ile Cys Leu Ala Lys Leu Arg
 340 345 350
 Ile Asp Pro Val Pro Pro Pro Asn Glu Phe Val Phe Asn His Trp Arg
 355 360 365
 Val Ser Tyr Ser Ser Cys Lys Tyr Ser His Leu Ile Thr Ser His Gln
 370 375 380
 Phe Gln Pro Ser Glu Leu Ile Lys Tyr Trp Asn His Leu Gln Gln Asn
 385 390 395 400
 Lys His Asn Ala Cys Ala Asn Ala Ala Lys Glu Lys Ala Gly Arg Tyr
 405 410 415
 Arg His Arg Lys Leu His
 420

<210> 12
 <211> 229
 <212> PRT
 <213> Artificial sequence

<220>
 <221> VARIANT
 <222> (1)...(229)
 <223> Xaa = Any Amino Acid

<400> 12
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 1 5 10 15
 Val Xaa Leu Xaa Xaa Xaa Phe Xaa Phe Leu Xaa His Trp Phe Phe Pro
 20 25 30
 Ile Trp Tyr Leu Ser Ile Pro Leu Arg Pro Gln Thr Gly Ser Xaa Ser
 35 40 45
 Xaa Ser Xaa Xaa Leu Ser His Leu Tyr Asn Thr Val Xaa Arg Xaa Asn
 50 55 60
 Xaa Xaa Phe Asn Asn Xaa Xaa Thr Arg Pro Ile Asn Ser Xaa Xaa Phe
 65 70 75 80
 Glu Phe Leu Ile Asp Glu Pro Xaa Lys Cys Xaa Lys Lys Pro Phe Leu
 85 90 95
 Val Leu Leu Ile Lys Ser Xaa Pro Gly Xaa Phe Xaa Ala Arg Gln Ala
 100 105 110
 Ile Arg Glu Thr Trp Gly Xaa Glu Xaa Asn Phe Xaa Gly Ile Xaa Val
 115 120 125
 Xaa Arg Val Phe Leu Leu Gly Lys Xaa Ala Glu Xaa Xaa Asp Pro Xaa
 130 135 140
 Leu Xaa Xaa Met Val Glu Xaa Glu Ser Arg Xaa His Gly Asp Ile Ile
 145 150 155 160
 Gln Gln Asp Phe Leu Asp Thr Tyr Phe Asn Leu Thr Leu Lys Thr Leu
 165 170 175
 Met Gly Met Arg Trp Val Ala Thr Phe Cys Pro Xaa Ala Glu Tyr Val
 180 185 190
 Met Lys Thr Asp Ser Asp Val Phe Val Asn Thr Xaa Asn Leu Leu Asn
 195 200 205
 Lys Leu Leu Lys Pro Ser Leu Ser His Arg Xaa Xaa Leu Phe Thr Gly
 210 215 220
 Tyr Val Ile Xaa Gly
 225

<210> 13
 <211> 1707
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (246)...(1436)

<221> misc_feature

<222> (1)...(1707)

<223> n = A,T,C or G

<400> 13

acgcgtccgc	gcagcggcag	cggcagcagc	ggcaacaagt	gccggagggt	agcagagcca	60
agccggagca	gtccctgccc	ccgacaccgc	cgggccgccc	gtccggggcg	ccgcgcattg	120
agcgtgagct	gcggcggctc	ccgggctgag	ccgcgcggag	cggccgggac	gtggatgtgg	180
ccgcgatctc	ccgcccttgc	ccccgccccg	ccgagctgga	gctgctccc	gacaagatat	240
gagaa atg agt gtt gga cgt cga aga ata aag ttg ttg ggt atc ctg atg						290
Met Ser Val Gly Arg Arg Arg Ile Lys Leu Leu Gly Ile Leu Met						
1	5		10		15	
atg gca aat gtc ttc att tat ttt att atg gaa gtc tcc aaa agc agt						338
Met Ala Asn Val Phe Ile Tyr Phe Ile Met Glu Val Ser Lys Ser Ser						
	20		25		30	
agc caa gaa aaa aat gga aaa ggg gaa gta ata ata ccc aaa gag aag						386
Ser Gln Glu Lys Asn Gly Lys Gly Glu Val Ile Ile Pro Lys Glu Lys						
	35		40		45	
ttc tgg aag ata tct acc cct ccc gag gca tac tgg aac cga gag caa						434
Phe Trp Lys Ile Ser Thr Pro Pro Glu Ala Tyr Trp Asn Arg Glu Gln						
	50		55		60	
gag aag ctg aac cgg cag tac aac ccc atc ctg agc atg ctg acc aac						482
Glu Lys Leu Asn Arg Gln Tyr Asn Pro Ile Leu Ser Met Leu Thr Asn						
	65		70		75	
cag acg ggg gag gcg ggc agg ctc tcc aat ata agc cat ctg aac tac						530
Gln Thr Gly Glu Ala Gly Arg Leu Ser Asn Ile Ser His Leu Asn Tyr						
	80		85		90	95
tgc gaa cct gac ctg agg gtc acg tcg gtg gtt acg ggt ttt aac aac						578
Cys Glu Pro Asp Leu Arg Val Thr Ser Val Val Thr Gly Phe Asn Asn						
	100		105		110	
ttg ccg gac aga ttt aaa gac ttt ctg ctg tat ttg aga tgc cgc aat						626
Leu Pro Asp Arg Phe Lys Asp Phe Leu Leu Tyr Leu Arg Cys Arg Asn						
	115		120		125	
tat tca ctg ctt ata gat cag ccg gat aag tgt gca aag aaa cct ttc						674
Tyr Ser Leu Leu Ile Asp Gln Pro Asp Lys Cys Ala Lys Lys Pro Phe						
	130		135		140	
ttg ttg ctg gcg att aag tcc ctc act cca cat ttt gcc aga agg caa						722
Leu Leu Leu Ala Ile Lys Ser Leu Thr Pro His Phe Ala Arg Arg Gln						
	145		150		155	
gca atc cgg gaa tcc tgg ggc caa gaa agc aac gca ggg aac caa acg						770
Ala Ile Arg Glu Ser Trp Gly Gln Glu Ser Asn Ala Gly Asn Gln Thr						
	160		165		170	175
gtg gtg cga gtc ttc ctg ctg ggc cag aca ccc cca gag gac aac cac						818
Val Val Arg Val Phe Leu Leu Gly Gln Thr Pro Pro Glu Asp Asn His						
	180		185		190	

ccc gac ctt tca gat atg ctg aaa ttt gag agt gag aag cac caa gac 866
 Pro Asp Leu Ser Asp Met Leu Lys Phe Glu Ser Glu Lys His Gln Asp
 195 200 205
 att ctt atg tgg aac tac aga gac act ttc ttc aac ttg tct ctg aag 914
 Ile Leu Met Trp Asn Tyr Arg Asp Thr Phe Phe Asn Leu Ser Leu Lys
 210 215 220
 gaa gtg ctg ttt ctc agg tgg gta agt act tcc tgc cca gac act gag 962
 Glu Val Leu Phe Leu Arg Trp Val Ser Thr Ser Cys Pro Asp Thr Glu
 225 230 235
 ttt gtt ttc aag ggc gat gac gat gtt ttt gtg aac acc cat cac atc 1010
 Phe Val Phe Lys Gly Asp Asp Asp Val Phe Val Asn Thr His His Ile
 240 245 250 255
 ctg aat tac ttg aat agt tta tcc aag acc aaa gcc aaa gat ctc ttc 1058
 Leu Asn Tyr Leu Asn Ser Leu Ser Lys Thr Lys Ala Lys Asp Leu Phe
 260 265 270
 ata ggt gat gtg atc cac aat gct gga cct cat cgg gat aag aag ctg 1106
 Ile Gly Asp Val Ile His Asn Ala Gly Pro His Arg Asp Lys Lys Leu
 275 280 285
 aag tac tac atc cca gaa gtt gtt tac tct ggc ctc tac cca ccc tat 1154
 Lys Tyr Tyr Ile Pro Glu Val Val Tyr Ser Gly Leu Tyr Pro Pro Tyr
 290 295 300
 gca ggg gga ggg ggg ttc ctc tac tcc ggc cac ctg gcc ctg agg ctg 1202
 Ala Gly Gly Gly Gly Phe Leu Tyr Ser Gly His Leu Ala Leu Arg Leu
 305 310 315
 tac cat atc act gac cag gtc cat ctc tac ccc att gat gac gtt tat 1250
 Tyr His Ile Thr Asp Gln Val His Leu Tyr Pro Ile Asp Asp Val Tyr
 320 325 330 335
 act gga atg tgc ctt cag aaa ctc ggc ctc gtt cca gag aaa cac aaa 1298
 Thr Gly Met Cys Leu Gln Lys Leu Gly Leu Val Pro Glu Lys His Lys
 340 345 350
 ggc ttc agg aca ttt gat atc gag gag aaa aac aaa aat aac atc tgc 1346
 Gly Phe Arg Thr Phe Asp Ile Glu Glu Lys Asn Lys Asn Asn Ile Cys
 355 360 365
 tcc tat gta gat ctg atg tta gta cat agt aga aaa cct caa gag atg 1394
 Ser Tyr Val Asp Leu Met Leu Val His Ser Arg Lys Pro Gln Glu Met
 370 375 380
 att gat att tgg tct cag ttg cag agt gct cat tta aaa tgc 1436
 Ile Asp Ile Trp Ser Gln Leu Gln Ser Ala His Leu Lys Cys
 385 390 395
 taaaatagat acaaaactcaa tttkgsatwg raagggggtwt tttgratwgg ycccatgttg 1496
 ggggtctcaca ttagagtaat ttctatttna ancatgaaat tgccttttatg agtgataccc 1556
 atttanggcc tctaancctt catttgnact cacgtgaaga agggaaagcg ggagaaggta 1616
 atttntttat ggtgaatggc aggatattgg tctgacttac cgntagggga ntttaaaact 1676
 ggnoccttttt gaatctgttt ggatggccct t 1707

<210> 14

<211> 397

<212> PRT
<213> Homo sapiens

<400> 14
Met Ser Val Gly Arg Arg Arg Ile Lys Leu Leu Gly Ile Leu Met Met
1 5 10 15
Ala Asn Val Phe Ile Tyr Phe Ile Met Glu Val Ser Lys Ser Ser Ser
20 25 30
Gln Glu Lys Asn Gly Lys Gly Glu Val Ile Ile Pro Lys Glu Lys Phe
35 40 45
Trp Lys Ile Ser Thr Pro Pro Glu Ala Tyr Trp Asn Arg Glu Gln Glu
50 55 60
Lys Leu Asn Arg Gln Tyr Asn Pro Ile Leu Ser Met Leu Thr Asn Gln
65 70 75 80
Thr Gly Glu Ala Gly Arg Leu Ser Asn Ile Ser His Leu Asn Tyr Cys
85 90 95
Glu Pro Asp Leu Arg Val Thr Ser Val Val Thr Gly Phe Asn Asn Leu
100 105 110
Pro Asp Arg Phe Lys Asp Phe Leu Leu Tyr Leu Arg Cys Arg Asn Tyr
115 120 125
Ser Leu Leu Ile Asp Gln Pro Asp Lys Cys Ala Lys Lys Pro Phe Leu
130 135 140
Leu Leu Ala Ile Lys Ser Leu Thr Pro His Phe Ala Arg Arg Gln Ala
145 150 155 160
Ile Arg Glu Ser Trp Gly Gln Glu Ser Asn Ala Gly Asn Gln Thr Val
165 170 175
Val Arg Val Phe Leu Leu Gly Gln Thr Pro Pro Glu Asp Asn His Pro
180 185 190
Asp Leu Ser Asp Met Leu Lys Phe Glu Ser Glu Lys His Gln Asp Ile
195 200 205
Leu Met Trp Asn Tyr Arg Asp Thr Phe Phe Asn Leu Ser Leu Lys Glu
210 215 220
Val Leu Phe Leu Arg Trp Val Ser Thr Ser Cys Pro Asp Thr Glu Phe
225 230 235 240
Val Phe Lys Gly Asp Asp Asp Val Phe Val Asn Thr His His Ile Leu
245 250 255
Asn Tyr Leu Asn Ser Leu Ser Lys Thr Lys Ala Lys Asp Leu Phe Ile
260 265 270
Gly Asp Val Ile His Asn Ala Gly Pro His Arg Asp Lys Lys Leu Lys
275 280 285
Tyr Tyr Ile Pro Glu Val Val Tyr Ser Gly Leu Tyr Pro Pro Tyr Ala
290 295 300
Gly Gly Gly Gly Phe Leu Tyr Ser Gly His Leu Ala Leu Arg Leu Tyr
305 310 315 320
His Ile Thr Asp Gln Val His Leu Tyr Pro Ile Asp Asp Val Tyr Thr
325 330 335
Gly Met Cys Leu Gln Lys Leu Gly Leu Val Pro Glu Lys His Lys Gly
340 345 350
Phe Arg Thr Phe Asp Ile Glu Glu Lys Asn Lys Asn Asn Ile Cys Ser
355 360 365
Tyr Val Asp Leu Met Leu Val His Ser Arg Lys Pro Gln Glu Met Ile
370 375 380
Asp Ile Trp Ser Gln Leu Gln Ser Ala His Leu Lys Cys
385 390 395

<210> 15
<211> 365
<212> PRT
<213> Homo sapiens

<400> 15
 Gln Glu Lys Asn Gly Lys Gly Glu Val Ile Ile Pro Lys Glu Lys Phe
 1 5 10 15
 Trp Lys Ile Ser Thr Pro Pro Glu Ala Tyr Trp Asn Arg Glu Gln Glu
 20 25 30
 Lys Leu Asn Arg Gln Tyr Asn Pro Ile Leu Ser Met Leu Thr Asn Gln
 35 40 45
 Thr Gly Glu Ala Gly Arg Leu Ser Asn Ile Ser His Leu Asn Tyr Cys
 50 55 60
 Glu Pro Asp Leu Arg Val Thr Ser Val Val Thr Gly Phe Asn Asn Leu
 65 70 75 80
 Pro Asp Arg Phe Lys Asp Phe Leu Leu Tyr Leu Arg Cys Arg Asn Tyr
 85 90 95
 Ser Leu Leu Ile Asp Gln Pro Asp Lys Cys Ala Lys Lys Pro Phe Leu
 100 105 110
 Leu Leu Ala Ile Lys Ser Leu Thr Pro His Phe Ala Arg Gln Ala
 115 120 125
 Ile Arg Glu Ser Trp Gly Gln Glu Ser Asn Ala Gly Asn Gln Thr Val
 130 135 140
 Val Arg Val Phe Leu Leu Gly Gln Thr Pro Pro Glu Asp Asn His Pro
 145 150 155 160
 Asp Leu Ser Asp Met Leu Lys Phe Glu Ser Glu Lys His Gln Asp Ile
 165 170 175
 Leu Met Trp Asn Tyr Arg Asp Thr Phe Phe Asn Leu Ser Leu Lys Glu
 180 185 190
 Val Leu Phe Leu Arg Trp Val Ser Thr Ser Cys Pro Asp Thr Glu Phe
 195 200 205
 Val Phe Lys Gly Asp Asp Asp Val Phe Val Asn Thr His His Ile Leu
 210 215 220
 Asn Tyr Leu Asn Ser Leu Ser Lys Thr Lys Ala Lys Asp Leu Phe Ile
 225 230 235 240
 Gly Asp Val Ile His Asn Ala Gly Pro His Arg Asp Lys Lys Leu Lys
 245 250 255
 Tyr Tyr Ile Pro Glu Val Val Tyr Ser Gly Leu Tyr Pro Pro Tyr Ala
 260 265 270
 Gly Gly Gly Gly Phe Leu Tyr Ser Gly His Leu Ala Leu Arg Leu Tyr
 275 280 285
 His Ile Thr Asp Gln Val His Leu Tyr Pro Ile Asp Asp Val Tyr Thr
 290 295 300
 Gly Met Cys Leu Gln Lys Leu Gly Leu Val Pro Glu Lys His Lys Gly
 305 310 315 320
 Phe Arg Thr Phe Asp Ile Glu Glu Lys Asn Lys Asn Asn Ile Cys Ser
 325 330 335
 Tyr Val Asp Leu Met Leu Val His Ser Arg Lys Pro Gln Glu Met Ile
 340 345 350
 Asp Ile Trp Ser Gln Leu Gln Ser Ala His Leu Lys Cys
 355 360 365

<210> 16

<211> 20

<212> DNA

<213> Homo sapiens

<220>

<221> Artificial sequence

<222> (1)...(20)

<223> Synthetically generated primer

<400> 16

cttcgacgcc ccacactcat

<210> 17
<211> 20
<212> DNA
<213> Homo sapiens

<220>
<221> Artificial sequence
<222> (1)...(20)
<223> Synthetically generated primer

<400> 17
atgagtgtgg ggcgtcgaag